

## Bacterial genes that make mercury deadly identified

**The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis.**

The sleepy fishing village of Minamata, Japan, 1956: physicians are baffled by a 5-year-old girl who has trouble walking and talking. Her suite of symptoms is like nothing the medics have seen before. Two days later, the girl's sister develops the same symptoms – and other cases quickly follow.

We now know that mercury poisoning was to blame: local industry had released the metal into the sea, where it accumulated in fish and shellfish as methylmercury – an organic form that is particularly easily absorbed by the body.

Methylmercury is now recognised as a neurotoxin, but we know little about it, other than that microbes make it from mercury, and that it builds up in animals further along the food chain, including us.

In 2013, a team at Oak Ridge National Laboratory in Tennessee [identified two genes –\*hgcA\* and \*hgcB\* – that seem to enable microbes to make the toxin](#). Now, that team, led by Mircea Podar, has looked for those genes in samples from a range of environments globally. Their work shows that methylmercury is produced by more bacterial types in a wider range of ecosystems than we thought.

“Some of the highest counts of the methylation genes were in melting permafrost, in Arctic Alaska,” says team member Dwayne Elias, also at Oak Ridge. This is worrying, he says, because with climate change, annual thaws will continue to let mercury pollution run off from melting snow into the tundra, where it can be converted into methylmercury.

**Read full, original post:** [Bacterial genes that turn mercury lethal mapped across world](#)